

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/509,121
Source: Pg110
Date Processed by STIC: 7/11/05

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PCT

RAW SEQUENCE LISTING DATE: 07/11/2005
 PATENT APPLICATION: US/10/509,121 TIME: 15:06:55

Input Set : A:\2005-05-31 1254-0259PUS1.ST25.txt
 Output Set: N:\CRF4\07112005\J509121.raw

3 <110> APPLICANT: Koichiro KAKU, et al.
 5 <120> TITLE OF INVENTION: GENE CODING FOR ACETOLACTATE SYNTHASE
 7 <130> FILE REFERENCE: 1254-0259PUS1
 9 <140> CURRENT APPLICATION NUMBER: US 10/509,121
 10 <141> CURRENT FILING DATE: 2004-09-28
 12 <150> PRIOR APPLICATION NUMBER: JP 2002-95721
 13 <151> PRIOR FILING DATE: 2002-03-29
 15 <160> NUMBER OF SEQ ID NOS: 39
 17 <170> SOFTWARE: PatentIn Ver. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2301
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Oryza sativa var. kinmaze
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (48)..(1979)
 28 <400> SEQUENCE: 1
 29 cccaaaccca gaaaccctcg ccggccggcgcc accccacc atg gct acg 56
 30 Met Ala Thr
 31 1
 33 acc gcc gcg gcc ggc ctg tcc gcc gcg acg gcc aag 104
 34 Thr Ala Ala Ala Ala Ala Ala Leu Ser Ala Ala Thr Ala Lys
 35 5 10 15
 37 acc ggc cgt aag aac cac cag cga cac cac gtc ctt ccc gct cga ggc 152
 38 Thr Gly Arg Lys Asn His Gln Arg His His Val Leu Pro Ala Arg Gly
 39 20 25 30 35
 41 cgg gtg ggg gcg gcg gtc agg tgc tcc gcg gtg tcc ccc gtc acc 200
 42 Arg Val Gly Ala Ala Ala Val Arg Cys Ser Ala Val Ser Pro Val Thr
 43 40 45 50
 45 ccg ccg tcc ccg gcg ccg ccc acg ccg ctc ccg ccg tgg ggg ccg 248
 46 Pro Pro Ser Pro Ala Pro Ala Thr Pro Leu Arg Pro Trp Gly Pro
 47 55 60 65
 49 gcc gag ccc cgc aag ggc gcg gac atc ctc gtg gag gcg ctg gag cgg 296
 50 Ala Glu Pro Arg Lys Gly Ala Asp Ile Leu Val Glu Ala Leu Glu Arg
 51 70 75 80
 53 tgc ggc gtc agc gac gtg ttc gcc tac ccg ggc gcg tcc atg gag 344
 54 Cys Gly Val Ser Asp Val Phe Ala Tyr Pro Gly Gly Ala Ser Met Glu
 55 85 90 95
 57 atc cac cag gcg ctg acg cgc tcc ccg gtc atc acc aac cac ctc ttc 392
 58 Ile His Gln Ala Leu Thr Arg Ser Pro Val Ile Thr Asn His Leu Phe
 59 100 105 110 115
 61 cgc cac gag cag ggc gag gcg ttc gcg gcg tcc ggg tac gcg cgc gcg 440
 62 Arg His Glu Gln Gly Glu Ala Phe Ala Ala Ser Gly Tyr Ala Arg Ala

P, b

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63	120	125	130	
65	tcc ggc cgc gtc ggg gtc tgc gtc gcc acc tcc ggc ccc ggg gca acc			488
66	Ser Gly Arg Val Gly Val Cys Val Ala Thr Ser Gly Pro Gly Ala Thr			
67	135	140	145	
69	aac ctc gtg tcc gcg ctc gcc gac gcg ctg ctc gac tcc gtc ccg atg			536
70	Asn Leu Val Ser Ala Leu Ala Asp Ala Leu Leu Asp Ser Val Pro Met			
71	150	155	160	
73	gtc gcc atc acg ggc cag gtc cac agc cgc atg atc ggc acc gac gcc			584
74	Val Ala Ile Thr Gly Gln Val His Ser Arg Met Ile Gly Thr Asp Ala			
75	165	170	175	
77	ttc cag gag acg ccc ata gtc gag gtc acc cgc tcc atc acc aag cac			632
78	Phe Gln Glu Thr Pro Ile Val Glu Val Thr Arg Ser Ile Thr Lys His			
79	180	185	190	195
81	aat tac ctt gtc ctt gat gtg gag gac atc ccc cgc gtc ata cag gaa			680
82	Asn Tyr Leu Val Leu Asp Val Glu Asp Ile Pro Arg Val Ile Gln Glu			
83	200	205	210	
85	gcc ttc ctc gcg tcc tcg ggc cgt cct ggc ccg gtg ctg gtc gac			728
86	Ala Phe Leu Ala Ser Ser Gly Arg Pro Gly Pro Val Leu Val Asp			
87	215	220	225	
89	atc ccc aag gac atc cag cag atg gcc gtg ccg gtc tgg gac acc			776
90	Ile Pro Lys Asp Ile Gln Gln Met Ala Val Pro Val Trp Asp Thr			
91	230	235	240	
93	tcg atg aat cta cca ggg tac atc gca cgc ctg ccc aag cca ccc gcg			824
94	Ser Met Asn Leu Pro Gly Tyr Ile Ala Arg Leu Pro Lys Pro Pro Ala			
95	245	250	255	
97	aca gaa ttg ctt gag cag gtc ttg cgt ctg gtt ggc gag tca cgg cgc			872
98	Thr Glu Leu Leu Glu Gln Val Leu Arg Leu Val Gly Glu Ser Arg Arg			
99	260	265	270	275
101	ccg att ctc tat gtc ggt ggt ggc tgc tct gca tct ggt gac gaa ttg			920
102	Pro Ile Leu Tyr Val Gly Gly Cys Ser Ala Ser Gly Asp Glu Leu			
103	280	285	290	
105	cgc tgg ttt gtt gag ctg act ggt atc cca gtt aca acc act ctg atg			968
106	Arg Trp Phe Val Glu Leu Thr Gly Ile Pro Val Thr Thr Leu Met			
107	295	300	305	
109	ggc ctc ggc aat ttc ccc agt gac gac ccg ttg tcc ctg cgc atg ctt			1016
110	Gly Leu Gly Asn Phe Pro Ser Asp Asp Pro Leu Ser Leu Arg Met Leu			
111	310	315	320	
113	ggg atg cat ggc acg gtg tac gca aat tat gcc gtg gat aag gct gac			1064
114	Gly Met His Gly Thr Val Tyr Ala Asn Tyr Ala Val Asp Lys Ala Asp			
115	325	330	335	
117	ctg ttg ctt gcg ttt ggt gtg cgg ttt gat gat cgt gtg aca ggg aaa			1112
118	Leu Leu Leu Ala Phe Gly Val Arg Phe Asp Asp Arg Val Thr Gly Lys			
119	340	345	350	355
121	att gag gct ttt gca agc agg gcc aag att gtg cac att gac att gat			1160
122	Ile Glu Ala Phe Ala Ser Arg Ala Lys Ile Val His Ile Asp Ile Asp			
123	360	365	370	
125	cca gca gag att gga aag aac aag caa cca cat gtg tca att tgc gca			1208
126	Pro Ala Glu Ile Gly Lys Asn Lys Gln Pro His Val Ser Ile Cys Ala			
127	375	380	385	

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129 gat gtt aag ctt gct tta cag ggc ttg aat gct ctg cta caa cag agc	1256
130 Asp Val Lys Leu Ala Leu Gln Gly Leu Asn Ala Leu Leu Gln Gln Ser	
131 390 395 400	
133 aca aca aag aca agt tct gat ttt agt gca tgg cac aat gag ttg gac	1304
134 Thr Thr Lys Thr Ser Ser Asp Phe Ser Ala Trp His Asn Glu Leu Asp	
135 405 410 415	
137 cag cag aag agg gag ttt cct ctg ggg tac aaa act ttt ggt gaa gag	1352
138 Gln Gln Lys Arg Glu Phe Pro Leu Gly Tyr Lys Thr Phe Gly Glu Glu	
139 420 425 430 435	
141 atc cca ccg caa tat gcc att cag gtg ctg gat gag ctg acg aaa ggt	1400
142 Ile Pro Pro Gln Tyr Ala Ile Gln Val Leu Asp Glu Leu Thr Lys Gly	
143 440 445 450	
145 gag gca atc atc gct act ggt gtt ggg cag cac cag atg tgg gcg gca	1448
146 Glu Ala Ile Ile Ala Thr Gly Val Gly Gln His Gln Met Trp Ala Ala	
147 455 460 465	
149 caa tat tac acc tac aag cgg cca cgg cag tgg ctg tct tcg gct ggt	1496
150 Gln Tyr Tyr Thr Tyr Lys Arg Pro Arg Gln Trp Leu Ser Ser Ala Gly	
151 470 475 480	
153 ctg ggc gca atg gga ttt ggg ctg cct gct gca gct ggt gct tct gtg	1544
154 Leu Gly Ala Met Gly Phe Gly Leu Pro Ala Ala Ala Gly Ala Ser Val	
155 485 490 495	
157 gct aac cca ggt gtc aca gtt gtt gat att gat ggg gat ggt agc ttc	1592
158 Ala Asn Pro Gly Val Thr Val Val Asp Ile Asp Gly Asp Gly Ser Phe	
159 500 505 510 515	
161 ctc atg aac att cag gag ctg gca ttg atc cgc att gag aac ctc cct	1640
162 Leu Met Asn Ile Gln Glu Leu Ala Leu Ile Arg Ile Glu Asn Leu Pro	
163 520 525 530	
165 gtg aag gtg atg gtg ttg aac aac caa cat ttg ggt atg gtg gtg caa	1688
166 Val Lys Val Met Val Leu Asn Asn Gln His Leu Gly Met Val Val Gln	
167 535 540 545	
169 tgg gag gat agg ttt tac aag gcg aat agg gcg cat aca tac ttg ggc	1736
170 Trp Glu Asp Arg Phe Tyr Lys Ala Asn Arg Ala His Thr Tyr Leu Gly	
171 550 555 560	
173 aac ccg gaa tgt gag agc gag ata tat cca gat ttt gtg act att gct	1784
174 Asn Pro Glu Cys Glu Ser Glu Ile Tyr Pro Asp Phe Val Thr Ile Ala	
175 565 570 575	
177 aag ggg ttc aat att cct gca gtc cgt gta aca aag aag agt gaa gtc	1832
178 Lys Gly Phe Asn Ile Pro Ala Val Arg Val Thr Lys Lys Ser Glu Val	
179 580 585 590 595	
181 cgt gcc gcc atc aag aag atg ctc gag act cca ggg cca tac ttg ttg	1880
182 Arg Ala Ala Ile Lys Lys Met Leu Glu Thr Pro Gly Pro Tyr Leu Leu	
183 600 605 610	
185 gat atc atc gtc ccg cac cag gag cat gtg ctg cct atg atc cca agt	1928
186 Asp Ile Ile Val Pro His Gln Glu His Val Leu Pro Met Ile Pro Ser	
187 615 620 625	
189 ggg ggc gca ttc aag gac atg atc ctg gat ggt gat ggc agg act gtg	1976
190 Gly Gly Ala Phe Lys Asp Met Ile Leu Asp Gly Asp Gly Arg Thr Val	
191 630 635 640	
193 tat taatctataa tctgtatgtt ggcaaaggcac cagcccgcc tatgtttgac	2029

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194 Tyr
 196 ctgaatgacc cataaaagagt ggtatgccta tgatgttgt atgtgctcta tcaataacta 2089
 198 aggtgtcaac tatgaaccat atgctcttct gtttacttg tttgatgtgc ttggcatgg 2149
 200 aatcctaatt agcttcctgc tgtcttaggtt tgttagtgtgt tggtttctgt agccatatgc 2209
 202 atcacaagat atcatgtaaag tttcttgc tacatatcaa taataagaga ataaagtact 2269
 204 tctatgcaaa aaaaaaaaaa aaaaaaaaaa aa 2301
 207 <210> SEQ ID NO: 2
 208 <211> LENGTH: 644
 209 <212> TYPE: PRT
 210 <213> ORGANISM: Oryza sativa var. kinmaze
 212 <400> SEQUENCE: 2
 213 Met Ala Thr Thr Ala Ala Ala Ala Ala Ala Leu Ser Ala Ala Ala
 214 1 5 10 15
 216 Thr Ala Lys Thr Gly Arg Lys Asn His Gln Arg His His Val Leu Pro
 217 20 25 30
 219 Ala Arg Gly Arg Val Gly Ala Ala Ala Val Arg Cys Ser Ala Val Ser
 220 35 40 45
 222 Pro Val Thr Pro Pro Ser Pro Ala Pro Pro Ala Thr Pro Leu Arg Pro
 223 50 55 60
 225 Trp Gly Pro Ala Glu Pro Arg Lys Gly Ala Asp Ile Leu Val Glu Ala
 226 65 70 75 80
 228 Leu Glu Arg Cys Gly Val Ser Asp Val Phe Ala Tyr Pro Gly Gly Ala
 229 85 90 95
 231 Ser Met Glu Ile His Gln Ala Leu Thr Arg Ser Pro Val Ile Thr Asn
 232 100 105 110
 234 His Leu Phe Arg His Glu Gln Gly Glu Ala Phe Ala Ala Ser Gly Tyr
 235 115 120 125
 237 Ala Arg Ala Ser Gly Arg Val Gly Val Cys Val Ala Thr Ser Gly Pro
 238 130 135 140
 240 Gly Ala Thr Asn Leu Val Ser Ala Leu Ala Asp Ala Leu Leu Asp Ser
 241 145 150 155 160
 243 Val Pro Met Val Ala Ile Thr Gly Gln Val His Ser Arg Met Ile Gly
 244 165 170 175
 246 Thr Asp Ala Phe Gln Glu Thr Pro Ile Val Glu Val Thr Arg Ser Ile
 247 180 185 190
 249 Thr Lys His Asn Tyr Leu Val Leu Asp Val Glu Asp Ile Pro Arg Val
 250 195 200 205
 252 Ile Gln Glu Ala Phe Phe Leu Ala Ser Ser Gly Arg Pro Gly Pro Val
 253 210 215 220
 255 Leu Val Asp Ile Pro Lys Asp Ile Gln Gln Gln Met Ala Val Pro Val
 256 225 230 235 240
 258 Trp Asp Thr Ser Met Asn Leu Pro Gly Tyr Ile Ala Arg Leu Pro Lys
 259 245 250 255
 261 Pro Pro Ala Thr Glu Leu Leu Glu Gln Val Leu Arg Leu Val Gly Glu
 262 260 265 270
 264 Ser Arg Arg Pro Ile Leu Tyr Val Gly Gly Gly Cys Ser Ala Ser Gly
 265 275 280 285
 267 Asp Glu Leu Arg Trp Phe Val Glu Leu Thr Gly Ile Pro Val Thr Thr
 268 290 295 300

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Output Set: N:\CRF4\07112005\J509121.raw

270 Thr Leu Met Gly Leu Gly Asn Phe Pro Ser Asp Asp Pro Leu Ser Leu
271 305 310 315 320
273 Arg Met Leu Gly Met His Gly Thr Val Tyr Ala Asn Tyr Ala Val Asp
274 325 330 335
276 Lys Ala Asp Leu Leu Ala Phe Gly Val Arg Phe Asp Asp Arg Val
277 340 345 350
279 Thr Gly Lys Ile Glu Ala Phe Ala Ser Arg Ala Lys Ile Val His Ile
280 355 360 365
282 Asp Ile Asp Pro Ala Glu Ile Gly Lys Asn Lys Gln Pro His Val Ser
283 370 375 380
285 Ile Cys Ala Asp Val Lys Leu Ala Leu Gln Gly Leu Asn Ala Leu Leu
286 385 390 395 400
288 Gln Gln Ser Thr Thr Lys Thr Ser Ser Asp Phe Ser Ala Trp His Asn
289 405 410 415
291 Glu Leu Asp Gln Gln Lys Arg Glu Phe Pro Leu Gly Tyr Lys Thr Phe
292 420 425 430
294 Gly Glu Glu Ile Pro Pro Gln Tyr Ala Ile Gln Val Leu Asp Glu Leu
295 435 440 445
297 Thr Lys Gly Glu Ala Ile Ile Ala Thr Gly Val Gly Gln His Gln Met
298 450 455 460
300 Trp Ala Ala Gln Tyr Tyr Thr Tyr Lys Arg Pro Arg Gln Trp Leu Ser
301 465 470 475 480
303 Ser Ala Gly Leu Gly Ala Met Gly Phe Gly Leu Pro Ala Ala Ala Gly
304 485 490 495
306 Ala Ser Val Ala Asn Pro Gly Val Thr Val Val Asp Ile Asp Gly Asp
307 500 505 510
309 Gly Ser Phe Leu Met Asn Ile Gln Glu Leu Ala Leu Ile Arg Ile Glu
310 515 520 525
312 Asn Leu Pro Val Lys Val Met Val Leu Asn Asn Gln His Leu Gly Met
313 530 535 540
315 Val Val Gln Trp Glu Asp Arg Phe Tyr Lys Ala Asn Arg Ala His Thr
316 545 550 555 560
318 Tyr Leu Gly Asn Pro Glu Cys Ser Glu Ile Tyr Pro Asp Phe Val
319 565 570 575
321 Thr Ile Ala Lys Gly Phe Asn Ile Pro Ala Val Arg Val Thr Lys Lys
322 580 585 590
324 Ser Glu Val Arg Ala Ala Ile Lys Lys Met Leu Glu Thr Pro Gly Pro
325 595 600 605
327 Tyr Leu Leu Asp Ile Ile Val Pro His Gln Glu His Val Leu Pro Met
328 610 615 620
330 Ile Pro Ser Gly Gly Ala Phe Lys Asp Met Ile Leu Asp Gly Asp Gly
331 625 630 635 640
333 Arg Thr Val Tyr
337 <210> SEQ ID NO: 3
338 <211> LENGTH: 2300
339 <212> TYPE: DNA
340 <213> ORGANISM: Oryza sativa var. kinmaze
342 <220> FEATURE:
343 <221> NAME/KEY: CDS

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/11/2005
PATENT APPLICATION: US/10/509,121 TIME: 15:06:56

Input Set : A:\2005-05-31_1254-0259PUS1.ST25.txt
Output Set: N:\CRF4\07112005\J509121.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:29; N Pos. 15

VERIFICATION SUMMARY

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Input Set : A:\2005-05-31 1254-0259PUS1.ST25.txt
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L:1545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0